RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/552,857_

Source: _Pu110_

Date Processed by STIC: _10/24/05_

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PCT

RAW SEQUENCE LISTING   DATE: 10/24/2005
PATENT APPLICATION: US/10/552,857   TIME: 10:50:34

Input Set : **A:\sequence.txt**
Output Set: **N:\CRF4\10242005\J552857.raw**

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     4 <110> APPLICANT: Agriculture Victoria Services Pty Ltd
     5        AgResearch Limited
     6        Spangenberg, German
     7        Emmerling, Michael
     8        Simmonds, Jason
     9        Winkworth, Amanda
    10        Panter, Stephen
    12 <120> TITLE OF INVENTION: Chlacone synthase dihydroflavonol-4-reductase and
    13        leucoanthrocyanidine reductase for clover, medic
    14        rygrass or fescue
    17 <130> FILE REFERENCE: FREE.P-007
C--> 20 <140> CURRENT APPLICATION NUMBER: US/10/552,857
C--> 20 <141> CURRENT FILING DATE: 2005-10-14
    20 <150> PRIOR APPLICATION NUMBER: 2003901797
    21 <151> PRIOR FILING DATE: 2003-04-14
    24 <150> PRIOR APPLICATION NUMBER: 2003904369
    25 <151> PRIOR FILING DATE: 2003-08-14
    28 <150> PRIOR APPLICATION NUMBER: PCT/AU2004/00494
W--> 29 <151> PRIOR FILING DATE: 2004-4-14
    32 <160> NUMBER OF SEQ ID NOS: 77
    35 <170> SOFTWARE: PatentIn version 3.2
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    39 <211> LENGTH: 1447
    40 <212> TYPE: DNA
    41 <213> ORGANISM: Trifolium repens
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    48 acgcatatta tatatatata tatatagtct ataattgaaa gaaactgcta aagatattat     120
    51 taagatatgg tgagtgtagc tgaaattcgc aaggctcaga gggctgaagg ccctgcaacc     180
    54 attttggcca ttggcactgc aaatccacca aaccgtgttg agcagagcac atatcctgat     240
    57 ttctacttca aaattacaaa cagtgagcac aagactgagc tcaaagagaa gttccaacgc     300
    60 atgtgtgaca aatccatgat caagagcaga tacatgtatc taacagaaga gattttgaaa     360
    63 gaaaatccta gtctttgtga atacatggca ccttcattgg atgctaggca agacatggtg     420
    66 gtggttgagg tacctagact tgggaaggag gctgcagtca aggccattaa agaatggggt     480
    69 caaccaaagt caaagattac tcacttaatc ttttgcacca caagtggtgt tgacatgcct     540
    72 ggtgctgatt accaactcac aaaactctta ggtcttcgcc catatgtgaa aaggtatatg     600
    75 atgtaccaac aaggttgttt tgcaggaggc acggtgcttc gtttggcaaa agatttggcc     660
    78 gagaacaaca aaggtgctcg tgtgctagtt gtttgttctg aagtcaccgc agtcacattt     720
    81 cgcggcccca gtgatactca cttggacagt cttgttggac aagcattgtt tggagatgga     780
    84 gccgctgcac taattgttgg ttctgatcca gtgcctgaaa ttgagaaacc aatatttgag     840
    87 atggtttgga ctgcacaaac aattgctcca gacagtgaag gtgccattga tggtcatctt     900
    90 cgtgaagctg ggctaacatt tcatcttctt aaagatgttc ctgggattgt atcaaagaac     960
    93 attaataaag cattggttga ggctttccaa ccattaggaa tttctgacta caactcaatc    1020
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99  ttgaagcccg aaaagatgag ggccacgagg gaagttctaa gtgaatatgg aaacatgtca    1140
102 agcgcatgtg tattgttcat cttagatgag atgcggaaga aatcggctca aaatggactt    1200
105 aagacaactg gagaaggact tgattggggt gtgttgttcg gcttcggacc aggacttacc    1260
108 attgaaaccg ttgttcttcg tagcgtggct atataagatg tgtgattgtt tttattttaa    1320
111 tgtattactt ttaatcttgc tgccttgaat ttcgatttaa gaataaataa atatatcttt    1380
114 tgataaaaaa aaaaaaaaaa aaaaaaaaa aagtactctg cgttgttacc actgcttaat     1440
117 cgaattc                                                              1447
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122 <211> LENGTH: 389
123 <212> TYPE: PRT
124 <213> ORGANISM: Trifolium repens
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140 Gln Ser Thr Tyr Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser Glu His
141         35                  40                  45
145 Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
146     50                  55                  60
150 Ile Lys Ser Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
151 65                  70                  75                  80
155 Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
156             85                  90                  95
160 Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Val Lys
161             100                 105                 110
165 Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
166         115                 120                 125
170 Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
171     130                 135                 140
175 Thr Lys Leu Leu Gly Leu Arg Pro Tyr Val Lys Arg Tyr Met Met Tyr
176 145                 150                 155                 160
180 Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
181             165                 170                 175
185 Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
186             180                 185                 190
190 Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
191         195                 200                 205
195 Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
196     210                 215                 220
200 Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
201 225                 230                 235                 240
205 Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
206             245                 250                 255
210 His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
211         260                 265                 270
215 Gly Ile Val Ser Lys Asn Ile Asn Lys Ala Leu Val Glu Ala Phe Gln
216         275                 280                 285
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220 Pro Leu Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
221     290                 295                 300
225 Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Gln Lys Leu Ala Leu Lys
226 305                 310                 315                 320
230 Pro Glu Lys Met Arg Ala Thr Arg Glu Val Leu Ser Glu Tyr Gly Asn
231             325                 330                 335
235 Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Lys
236             340                 345                 350
240 Ser Ala Gln Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly
241         355                 360                 365
245 Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu
246     370                 375                 380
250 Arg Ser Val Ala Ile
251 385
255 <210> SEQ ID NO: 3
256 <211> LENGTH: 2394
257 <212> TYPE: DNA
258 <213> ORGANISM: Trifolium repens
261 <400> SEQUENCE: 3
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265 aaattcactc attgcataga aaaccataca catttgatct tgcaaagaag aaatatggga    120
268 gacgaaggta tagtgagagg tgtcacaaag cagacaaccc ctgggaaggc tactatattg    180
271 gctcttggca aggcattccc tcaccaactt gtgatgcaag agtgtttagt tgatggttat    240
274 tttagggaca ctaattgtga caatcctgaa cttaagcaga aacttgctag actttgtaag    300
277 acaaccacgg taaaaacaag gtatgttgtt atgaatgagg agatactaaa gaaatatcca    360
280 gaacttgttg tcgaaggcgc ctcaactgta aaacaacgtt tagagatatg taatgaggca    420
283 gtaacacaaa tggcaattga agcttcccaa gtttgcctaa agaattgggg tagatcctta    480
286 tcggacataa ctcatgtggt ttatgtttca tctagtgaag ctagattacc cggtggtgac    540
289 ctatacttgt caaaaggact aggactaaac cctaaaattc aaagaaccat gctctatttc    600
292 tctggatgct cgggaggcgt agccggcctt cgcgttgcga aagacgtagc tgagaacaac    660
295 cctggaagta gagttttgct tgctacttcg gaaactacaa ttattggatt caagccacca    720
298 agtgttgata gaccttatga tcttgttggt gtggcactct ttggagatgg tgctggtgca    780
301 atgataattg gctcagaccc ggtatttgaa actgagacac cattgtttga gctgcatact    840
304 tcagctcagg agtttatacc agacaccgag aagaaaattg atgggcggct gacggaggag    900
307 ggcataagtt tcacactagc aagggaactt ccgcagataa tcgaagacaa tgttgaggga    960
310 ttctgtaata aactaattga tgttgttggg ttggagaata aggagtacaa taagttgttt   1020
313 tgggctgtgc atccaggtgg gcctgcgata ttgaatcgcg tggagaagcg gcttgagttg   1080
316 tcgccgcaga agctgaatgc tagtagaaaa gctctaatgg attatggaaa tgctagcagc   1140
319 aatactattg tttatgtgct ggaatatatg ctagaagagg aaaagaagat taaaaaggcg   1200
322 ggtggaggag attctgaatg gggattgata cttgcttttg gacctggaat tactttgag    1260
325 gggattctag caaggaactt gtgtgcatga agtcttatac aattgtgatg catgacttat   1320
328 actcttattt ctactaatta ttatattaag caaattcaga actttttaagt aatgatttaa   1380
331 tgaagaatac ttatagtata ttgactttat tcactttcaa agcaagttta tgatcctaag   1440
334 acatggtaga acttgagcat gtggaatagt tgtaacaaaa actctaagca aatagagact   1500
337 ttatgtagta taaagcattt ccagacatga taaataatgg tacctcagaa cataaaatat   1560
340 atttagctat cttttcatccc caactttaca catccaccaa ggtacagaat aagcatatgt   1620
343 caacacaaaa tgtactctaa gtctaacatg agtaaccaaa catgatgcct gattaagtta   1680
346 aaagaaaaga aaatctgagg gcatagatct tcaatcacac cactccagag ggaaggcgta   1740
349 gaacaagctg tccgccgaaa acactgcaat tcaataaata tcattaggac aacagtgcag   1800
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358 tgagataaga accatgacgg ccataagcca taccccaagg caaccaataa atgtccacgg  1980
361 gtatctaaca cctgttgcaa gaaatagtaa gttattagga gatgtgcggt tacgaaattc  2040
364 aagctacaca acaaaaggag gccagaacaa cagcaatctt gtaaccagat gacaacaata  2100
367 aaatgtaaac ttaaagagac cgaacacaca aacattgcaa ctcagatgga attgctgcca  2160
370 tgtaactagt aggagatttg ggacgtcaaa tcagtatatt atgcaaatac aaggtatgac  2220
373 cgccttgtct attgtagcat acaacaaacg tacagtgggt ttgtccctct caaaatggca  2280
376 ggatctttac agcacaatat ttggttttgt catacttata ccataaaaaa aaaaaaaaa  2340
379 aaaaaaaaaa aaagtactct gcgttgttac cactgcttaa tcactagtga attc         2394
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384 <211> LENGTH: 391
385 <212> TYPE: PRT
386 <213> ORGANISM: Trifolium repens
389 <400> SEQUENCE: 4
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393 1               5                   10                  15
397 Gly Lys Ala Thr Ile Leu Ala Leu Gly Lys Ala Phe Pro His Gln Leu
398                 20                  25                  30
402 Val Met Gln Glu Cys Leu Val Asp Gly Tyr Phe Arg Asp Thr Asn Cys
403             35                  40                  45
407 Asp Asn Pro Glu Leu Lys Gln Lys Leu Ala Arg Leu Cys Lys Thr Thr
408         50                  55                  60
412 Thr Val Lys Thr Arg Tyr Val Val Met Asn Glu Glu Ile Leu Lys Lys
413 65                  70                  75                  80
417 Tyr Pro Glu Leu Val Val Glu Gly Ala Ser Thr Val Lys Gln Arg Leu
418                 85                  90                  95
422 Glu Ile Cys Asn Glu Ala Val Thr Gln Met Ala Ile Glu Ala Ser Gln
423             100                 105                 110
427 Val Cys Leu Lys Asn Trp Gly Arg Ser Leu Ser Asp Ile Thr His Val
428             115                 120                 125
432 Val Tyr Val Ser Ser Ser Glu Ala Arg Leu Pro Gly Gly Asp Leu Tyr
433         130                 135                 140
437 Leu Ser Lys Gly Leu Gly Leu Asn Pro Lys Ile Gln Arg Thr Met Leu
438 145                 150                 155                 160
442 Tyr Phe Ser Gly Cys Ser Gly Gly Val Ala Gly Leu Arg Val Ala Lys
443             165                 170                 175
447 Asp Val Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Leu Ala Thr Ser
448             180                 185                 190
452 Glu Thr Thr Ile Ile Gly Phe Lys Pro Pro Ser Val Asp Arg Pro Tyr
453         195                 200                 205
457 Asp Leu Val Gly Val Ala Leu Phe Gly Asp Gly Ala Gly Ala Met Ile
458     210                 215                 220
462 Ile Gly Ser Asp Pro Val Phe Glu Thr Glu Thr Pro Leu Phe Glu Leu
463 225                 230                 235                 240
467 His Thr Ser Ala Gln Glu Phe Ile Pro Asp Thr Glu Lys Lys Ile Asp
468             245                 250                 255
472 Gly Arg Leu Thr Glu Glu Gly Ile Ser Phe Thr Leu Ala Arg Glu Leu
473             260                 265                 270
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477 Pro Gln Ile Ile Glu Asp Asn Val Glu Gly Phe Cys Asn Lys Leu Ile
478         275                 280                 285
482 Asp Val Val Gly Leu Glu Asn Lys Glu Tyr Asn Lys Leu Phe Trp Ala
483     290                 295                 300
487 Val His Pro Gly Gly Pro Ala Ile Leu Asn Arg Val Glu Lys Arg Leu
488 305                 310                 315                 320
492 Glu Leu Ser Pro Gln Lys Leu Asn Ala Ser Arg Lys Ala Leu Met Asp
493             325                 330                 335
497 Tyr Gly Asn Ala Ser Ser Asn Thr Ile Val Tyr Val Leu Glu Tyr Met
498             340                 345                 350
502 Leu Glu Glu Glu Lys Lys Ile Lys Lys Ala Gly Gly Gly Asp Ser Glu
503             355                 360                 365
507 Trp Gly Leu Ile Leu Ala Phe Gly Pro Gly Ile Thr Phe Glu Gly Ile
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530 gatttgaatg gaagttcctc ggtgaatgga gcacgtgcta gacgtgctcc tactcaggga    180
533 aaggcaacga tacttgcatt aggaaaggct ttccccgccc aggtcctccc tcaagagtgc    240
536 ttggtggaag gattcattcg cgacactaag tgtgacgata cttatattaa ggagaaattg    300
539 gagcgtcttt gcaaaaacac aactgtgaaa acaagataca cagtaatgtc aaaggagatc    360
542 ttagacaact atccagagct agccatagat ggaacaccaa caataaggca aaagcttgaa    420
545 atagcaaatc cagcagtagt tgaaatggca acaagagcaa gcaaagattg catcaaagaa    480
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569 agaatcactg aagagggtat taattttaag cttggaagag accttcctca aaaaattgaa    960
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575 gacttatttt gggctgttca tcctggtggg ccagctatac tcaataagct agaaaatata   1080
578 ctcaaattga aaagtgataa attggattgt agtaggaagg cattaatgga ttatggaaat   1140
581 gttagtagca atactatatt ctatgtgatg gagtatatga gagattattt gaaggaagat   1200
584 ggaagtgaag aatggggatt aggattggct tttggaccag ggattacttt tgaaggggtt   1260
587 ctcctccgta gcctttaatc ttgaaataat aattcatatg aaattacttg tcttaagatt   1320
590 gtgataggaa gatgaatatg tattggatta atattgatat ggtgttattt taagttgatt   1380
593 ttaaaaaaag tttattaata aagtatgatg taacaattgt tgtttgaatg ttaaaaggga   1440
596 agtatactat tttaagttct tgaccatact gatttttct ttacacattt tcatatctaa   1500
599 aattgttcta tgatatcttc attgttgata ctgtaataat ataatatcta atttggctgg   1560
602 caaaatgaaa gatttttcac cgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagtactctg   1620
605 cgttgttacc actgcttaat cactagtgaa ttc                                1653
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/24/2005
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Input Set : A:\sequence.txt
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<u>Invalid <213> Response:</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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Seq#:65,66,67,68,69,70,71,72,73,74,75,76,77

VERIFICATION SUMMARY   DATE: 10/24/2005
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Input Set : **A:\sequence.txt**
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L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:29 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
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